

Package ‘sdmApp’

July 7, 2021

Title A User-Friendly Application for Species Distribution Modeling

Version 0.0.2

Author Aboubacar HEMA [aut, cre],
Babacar NDAO [aut],
Louise LEROUX [aut],
Abdoul Aziz DIOUF [aut]

Maintainer Aboubacar HEMA <aboubacarhema94@gmail.com>

Description A 'shiny'
application that allows non-expert 'R' users to easily model
species distribution. It offers a reproducible work flow for
species distribution modeling into a single and user friendly environment.
'sdmApp' takes 'raster' data (in format supported by the 'raster package')
and species occurrence data (several format supported) as input argument.
It provides an interactive graphical user interface (GUI).

License GPL-3

URL <https://github.com/Abson-dev/sdmApp>

BugReports <https://github.com/Abson-dev/sdmApp/issues>

Depends R (>= 3.5.0)

Imports raster (>= 2.6.7), sp (>= 1.2.0), shiny (>= 0.12.2)

Suggests covr, grDevices, knitr, rmarkdown, stats, testthat, utils,
rgdal (>= 1.5-8), automap (>= 1.0-14), future.apply, blockCV
(>= 2.1.1), dismo (>= 1.0.12), DT, kernlab (>= 0.9-29),
randomForest (>= 4.6.10), readxl (>= 1.3.1), rhandsontable (>=
0.3.7), sf, shinyBS (>= 0.61), shinyFiles (>= 0.7.0), SSDM (>=
0.2.8), ggcorrplot (>= 0.1.3), ggplot2 (>= 3.1.1), cowplot (>=
1.1.1), haven (>= 2.3.1), dplyr (>= 1.0.3), tidyr (>= 1.1.2),
data.table, rgeos (>= 0.3-8), rJava (>= 0.9-13)

VignetteBuilder knitr, rmarkdown

Encoding UTF-8

Language en-US

LazyLoad yes

LazyData no
ZipData no
BuildResaveData no
RoxygenNote 7.1.1
SystemRequirements Java (>= 8)
NeedsCompilation no
Repository CRAN
Date/Publication 2021-07-07 08:30:02 UTC

R topics documented:

| | |
|--------------------------------|----------|
| sdmApp | 2 |
| sdmApp_fold_Explorer | 3 |
| sdmApp_PA | 4 |
| sdmApp_RasterPlot | 4 |
| sdmApp_TimesRasters | 5 |
| Index | 6 |

| | |
|--------|--|
| sdmApp | <i>starts the graphical user interface developed with shiny.</i> |
|--------|--|

Description

starts the graphical user interface developed with shiny.

Usage

```
sdmApp(
  maxRequestSize = 50,
  debug = FALSE,
  theme = "IHSN",
  ...,
  shiny.server = FALSE
)
```

Arguments

| | |
|----------------|--|
| maxRequestSize | (numeric) number defining the maximum allowed file size (in megabytes) for uploaded files, defaults to 50MB |
| debug | logical if TRUE, set shiny-debugging options |
| theme | select style sheet for the interface. |
| ... | arguments (e.g host) that are passed through runApp when starting the shiny application |
| shiny.server | Setting this parameter to TRUE will return the app in the form of an object rather than invoking it. This is useful for deploying sdmApp via shiny-server. |

Value

starts the interactive graphical user interface.

Examples

```
if(interactive()){
#load the package
library(sdmApp)
sdmApp()
}
```

sdmApp_fold_Explorer *Explore the generated folds and visualize the placement of folds and distribution of species data over folds.*

Description

Explore the generated folds and visualize the placement of folds and distribution of species data over folds.

Usage

```
sdmApp_fold_Explorer(blocks, rasterLayer, speciesData, num)
```

Arguments

| | |
|-------------|---|
| blocks | A SpatialBlock object. |
| rasterLayer | A raster object as background map for visualization. |
| speciesData | A simple features (sf) or SpatialPoints object containing species data (response variable). |
| num | A number of fold to assign as data test set. |

Value

A map showing folds and the species data, that can be used to explore folds.

Examples

```
## Not run:
# load blockCV package data
library(blockCV)
awt <- raster::brick(system.file("extdata", "awt.grd", package = "blockCV"))
#import presence-absence species data
PA <- read.csv(system.file("extdata", "PA.csv", package = "blockCV"))
#make a sf object from data.frame
pa_data <- sf::st_as_sf(PA, coords = c("x", "y"), crs = raster::crs(awt))
#spatial blocking by specified range and random assignment
sb <- spatialBlock(speciesData = pa_data, species = "Species",
```

```
rasterLayer = awt,theRange = 70000,k = 5,  
selection = "random",iteration = 100)  
sdmApp_fold_Explorer(sb,awt,pa_data,1)  
  
## End(Not run)
```

sdmApp_PA *Plot presence/absence map*

Description

Plot presence/absence map

Usage

```
sdmApp_PA(x)
```

Arguments

x Raster object

Value

a ggplot object

Examples

```
r <- raster::raster(system.file("extdata","AETI.tif",package = "sdmApp"))  
r <- r > 4000  
sdmApp_PA(r)
```

sdmApp_RasterPlot *Plot a raster*

Description

Plot a raster

Usage

```
sdmApp_RasterPlot(x)
```

Arguments

x Raster object

Value

a ggplot object

Examples

```
r <- raster::raster(system.file("extdata", "AETI.tif", package = "sdmApp"))
sdmApp_RasterPlot(r)
```

sdmApp_TimesRasters *Multiply the probability of occurrence map with the presence/absence map to get a presence map only.*

Description

Multiply the probability of occurrence map with the presence/absence map to get a presence map only.

Usage

```
sdmApp_TimesRasters(x, y)
```

Arguments

| | |
|---|--|
| x | Probability of occurrence map, a Raster object |
| y | Presence/Absence map, a Raster object |

Value

Probability of occurrence map with only presence

Examples

```
r <- raster::raster(system.file("extdata", "AETI.tif", package = "sdmApp"))
r2 <- r > raster::cellStats(r, stat='mean', na.rm=TRUE)
r <- r/raster::maxValue(r)
names(r) <- "propability of occurrence"
z<-sdmApp_TimesRasters(r,r2)
sdmApp_RasterPlot(z)
```

Index

[runApp](#), [2](#)

[sdmApp](#), [2](#)

[sdmApp_fold_Explorer](#), [3](#)

[sdmApp_PA](#), [4](#)

[sdmApp_RasterPlot](#), [4](#)

[sdmApp_TimesRasters](#), [5](#)